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OM nucleic - nucleic search, using sw model

Run on: June 24, 1999, 00:38:04 ; Search time 67.43 seconds
(without alignments)
25.110 Million cell updates/sec

Title: US-09-205-015-1

Perfect score: 9

Sequence: 1 totgagtc 9

Scoring table: IDENTITY_NUC

Searched: 240622 seqs, 94065609 residues

Database : N_Geneseq_34:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	9 100.0	9170	1	Q02829	DNA complementary
2	9 100.0	1212	1	Q03739	Arginine deaminase
3	9 100.0	4320	1	N90349	Transcription sequ
4	9 100.0	814	1	N90393	Human interleukin-
5	9 100.0	3622	1	N90567	Ovine Y-chromosoma
6	9 100.0	816	1	N90228	DNA encoding inter
7	9 100.0	864	1	N90283	Human interleukin-
8	9 100.0	1589	1	N90342	DNA of wild-type h
9	9 100.0	1569	1	N90343	DNA of mutant huma
10	9 100.0	2120	1	N92440	DNA sequence encod
11	9 100.0	9473	1	N92768	HIV-2 variant HIV-
12	9 100.0	2100	1	N90352	Sequence of plasmid
13	9 100.0	1920	1	N90353	Sequence of plasmid
14	9 100.0	4729	1	Q04043	Recombinant DNA fo
15	9 100.0	402	1	Q05114	HIV-1 protease gen
16	9 100.0	535	1	Q05115	HIV-1 protease gen
17	9 100.0	375	1	Q05116	HIV-1 protease gen
18	9 100.0	2520	1	N81459	C3 mutant gene enc
19	9 100.0	2946	1	N81458	Hra mutant gene en
20	9 100.0	60	1	N81999	Adenovirus transcr
21	9 100.0	582	1	N82002	Restriction fragme
22	9 100.0	9229	1	N80437	Entire sequence of
23	9 100.0	3031	1	N81541	Sequence of pcps-5
24	9 100.0	3861	1	Q05979	Recombinant AcNPV-
25	9 100.0	4113	1	Q06644	Recombinant AcNPV-
26	9 100.0	1883	1	Q05748	EPO receptor gene.
27	9 100.0	1770	1	Q06266	Promoter region an
28	9 100.0	2184	1	Q06301	Sequence encoding
29	9 100.0	3081	1	Q05876	pgp5-5 plasmid seq
30	9 100.0	2466	1	Q06903	Sequence encoding
31	9 100.0	5468	1	Q06540	Human low density
32	9 100.0	2400	1	N70061	5' region of human
33	9 100.0	5522	1	N70062	Sau3A-EcoRI 5.4 kb
34	9 100.0	816	1	Q03406	Sequence of plasmid
35	9 100.0	3874	1	N70225	Sequence of genom
36	9 100.0	1431	1	N70264	Sequence encoding
37	9 100.0	8247	1	N70996	Sequence encoding
38	9 100.0	5340	1	N71017	Sequence of LAV/HT
39	9 100.0	1395	1	Q11248	Tryptophanase gene
40	9 100.0	3540	1	Q11854	Glutamate receptor
41	9 100.0	2280	1	N91142	Sequence of plasmid
42	9 100.0	2930	1	Q11494	Tobacco SURB-Hra m
43	9 100.0	2520	1	Q11495	Tobacco SURA-C3 mu

Versican gene. Ver
Human secreted pro

ALIGNMENTS

RESULT 1.	
Q02829	Q02829 standard; DNA; 9170 BP.
AC	Q02829;
DT	12-JUN-1990 (first entry)
DE	DNA complementary to simian immunodeficiency virus
KW	SIV; simian immunodeficiency virus; AIDS; HIV; vaccine; ss.
OS	SIV.
PH	Key.
FT	5'utr
FT	118..431
FT	/*tag= a
FT	220..237
FT	/*tag= b
FT	432..1988
FT	/*tag= c
FT	/label-gag gene
FT	1634..4816
FT	/*tag= d
FT	/label-pol gene
FT	4755..5459
FT	/*tag= e
FT	/label-Q gene
FT	5236..5592
FT	/*tag= f
FT	/label-X gene
FT	5546..8085
FT	/*tag= g
FT	/label-tat gene
FT	5703..8174
FT	/*tag= h
FT	/label-art gene
FT	5765..7983
FT	/*tag= i
FT	/label-SD to SA
FT	5770..8076
FT	/*tag= j
FT	/label-env gene
FT	8080..8364
FT	/*tag= k
FT	/label-F gene
FT	8201..9153
FT	/*tag= l
FT	3'utr
PN	J01289485-A.
PD	21-NOV-1989.
PF	16-JUN-1988; 119023
PR	16-JUN-1988; JP-119023.
PA	(TOFU) Toa Nenryo Kogyo KK.
DR	WPI; 90-005176/01.
DR	P-PSDB; R04191-99.
PT	DNA complementary to RNA of simian immuno-deficiency virus -
PT	used in vaccines and for diagnosis of AIDS.
PS	Disclosure; Fig 4; 6pp; Japanese.
CC	Sequence complementary to RNA of SIV from which vector plasmid pSAH121
CC	may be constructed and incorporated into an E.coli vector. Useful in
CC	developing a vaccine against and in diagnosis of AIDS.
CC	Feature marked as intron is not described in the specification as such,
CC	but divides the tat and art genes between 5762-7984 and 5763-7985
CC	respectively.
CC	The 3'UTR has a short coding region associated with it in the
CC	specification.
SQ	Sequence 9170 BP; 3171 A; 1719 C; 2265 G; 2014 T; 1 Others;

Query Match 100.0%; Score 9; DB 1; Length 9170;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 tctgagtcga 9
DB 124 TCTGAGTCA 132

RESULT 2
Q03739/C
ID Q03739 standard; DNA; 1212 BP.
AC Q03739;
DE Arginine deaminase (first entry)
DE Arginine deaminase encoding gene.
KW Arginine deaminase; carcinostatic; cancer; ds.
PN J02053490-A.
PD 22-FEB-1990.
PF 16-AUG-1988; 202759.
PR 16-AUG-1988; JP-202759.
PA (AGEN) Agency of Ind Sci Tech.
DR WPI: 90-103119/14.
DR P-PSDB: R05713.
PT Arginine deaminase gene -
PT where DNA contains base sequence that codes amino acid sequence
PT of arginine deaminase composing polypeptide.
PS Disclosure: Fig 2; 18pp; Japanese.
CC Expression vector transformed by the gene may be used to produce large
CC quantities of arginine deaminase, useful as a carcinostatic.
SQ Sequence 1212 BP; 463 A; 190 C; 192 G; 367 T;

Query Match 100.0%; Score 9; DB 1; Length 1212;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtcga 9
DB 305 TCTGAGTCA 297

RESULT 3
N90349/C
ID N90349 standard; DNA; 4320 BP.
AC N90349;
DE Transcription sequence of plasmid pUC19BgEc2
DE pUC19BgEc2; HIV; pol region; HIV protease.
OS Human immunodeficiency virus
FH Key Location/Qualifiers
FT cds 1..4320
FT /*tag= a
PN DE3800233-A.
PD 20-JUL-1989.
PF 07-JAN-1988; 00233.
PR 07-JAN-1988; DE-800233;
PA (WOLF) Hans Wolf.
PI Wolf H, Soutschek-Bauer E, Motz M;
DR WPI: 89-213869/30.
PT DNA coding for HIV protease and polypeptide precursor - useful for
PT screening for specific HIV protease inhibitors.
PS Disclosure: fig. 2; page 12-18; 36pp; german.
CC The plasmid contains the entire pol reading frame (protease, reverse
CC transcriptase and endonuclease). See P91048.
SQ Sequence 4320 BP; 1657 A; 736 C; 985 G; 942 T;

Query Match 100.0%; Score 9; DB 1; Length 4320;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtcga 9
DB 517 TCTGAGTCA 509

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RESULT 4
N90393/C
ID N90393 standard; cDNA; 814 BP.
AC N90393;
DT 20-OCT-1989 (first entry)
DE Human interleukin-1 (alpha-type) cDNA.
KW Human interleukin-1 (alpha-type); cDNA; prostaglandin E2;
KW lymphocyte activation.
OS Homo sapiens (human)
FH Key Location/Qualifiers
FT cds 1..811
FT /*tag= a
PN EP-327360-A.
PD 09-AUG-1989.
PF 02-FEB-1989; 301007.
PR 03-FEB-1988; JP-024613.
PA (DAIN) Dainippon Pharm KK.
PI Yamagishi J, Kotani H, Furuta R, Fukui T;
DR WPI: 89-229370/32.
DR P-PSDB: P90535, P90472, P90473, P90474.
PT Modified human interleukin-1 polypeptide(s)
PT - show almost no induction of prodn. of prostaglandin E2 while
PT activating lymphocytes.
PS Disclosure: table 8, page 16-18; 24pp; English.
CC Human interleukin-1 (alpha-type) cDNA. Produces peptides
CC which can be modified (see P90535-translaction; P90472-4-for
CC modified peptides). These peptides show almost no induction
CC of the prodn. of prostaglandin E2, while they show activation of
CC lymphocytes.
SQ Sequence 814 BP; 257 A; 187 C; 171 G; 199 T;

Query Match 100.0%; Score 9; DB 1; Length 814;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtcga 9
DB 312 TCTGAGTCA 304

RESULT 5
N90567/C
ID N90567 standard; DNA; 3622 BP.
AC N90567;
DT 14-MAR-1990 (first entry)
DE Ovine Y-chromosomal DNA repeat element OY4.1-4.2.
KW PCR; Y-chromosome; repeat; sex determination.
OS Ovis aries
FH Key Location/Qualifiers
FT misc_feature 1..1076
FT /*tag= a
FT misc_feature 1077..3622
FT /*tag= b
PN W08907154-A.
PD 10-AUG-1989.
PF 27-JAN-1989; AU6476.
PR 23-JAN-1988; AU-PI6476.
PA (ADRI) Advanced Riverina Holdings Ltd.
PI Reed KC, Lord EA, Matthei KI, Mann DA, Beaton S;
DR WPI: 89-249021/34.
PT New nucleic acid isolates hybridising only ruminant Y chromosomal DNA
PT - useful in hybridisation and polymerase chain reaction tests for sex
PT determination.
PS Disclosure: fig.2; 120pp; English.
CC The sequence encodes ovine Y-specific chromosomal repeat element
CC OY4.1-4.2. OY4.2 (tag a) and OY9.1 (tag b) are BamHI-BamHI and
CC HindIII-BamHI restriction fragments resp., from bacteriophage
CC lambda(OY4). They are conserved, male-specific, and repeated in
CC ruminants. They are useful in hybridisation and polymerase chain
CC reaction tests for sex determination in ruminants.
SQ Sequence 3622 BP; 803 A; 1049 C; 930 G; 840 T; 0 Others;

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Query Match      100.0%; Score 9; DB 1; Length 3622;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtca 9
   |||||
Db 2744 TCTGAGTCA 2736

RESULT 6
N90228/c
ID N90228 standard; DNA; 816 BP.
AC N90228;
DE DNA encoding interleukin 1 and its prosequence.
KW DNA; prosequence; protein; human interleukin 1.
OS Homo sapiens (Human)
FH Key Location/Qualifiers
FT cds 336..813
   /*tag= b
FT signal_peptide 1..335
   /*tag= c
FT J01137977-A.
PN 24-MAY-1989.
PD 19-NOV-1987; 292739.
PF 19-NOV-1987; JP-292739.
PR (DAIN) Dainippon Pharm KK.
PA WPI: 89-198222/27.
DR P-PSDB; P90421.
DE High phenotypic expression plasmid
   - for prodn. of human interleukin 1 polypeptide.
PS Disclosure: fig 5; 10pp; Japanese.
CC DNA encoding interleukin 1 and its prosequence (see P90421). Used to
   produce human interleukin 1.
SQ Sequence 816 BP; 257 A; 187 C; 171 G; 201 T;

Query Match      100.0%; Score 9; DB 1; Length 816;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtca 9
   |||||
Db 314 TCTGAGTCA 306

RESULT 7
N90283/c
ID N90283 standard; DNA; 864 BP.
AC N90283;
DE 1-NOV-1989 (first entry)
DE Human interleukin-1 alpha polypeptide(s).
KW Interleukin-1 alpha; immunostimulant.
OS Homo sapiens
FH Key Location/Qualifiers
FT cds 37..849
   /*tag= a
FT 385..849
   /*tag= b
FT EP-324447-A.
PN 19-JUL-1989.
PD 11-JAN-1989; 100402.
PF 15-JAN-1988; US-144457.
PR (HOFF) F Hoffmann-La Roche & Co.
PA Lomedito PT;
PI WPI: 89-208412/29.
DR P-PSDB; P90108.
DE New recombinant human interleukin-1 alpha polypeptide(s) - without
   N-terminal methionine residue, useful e.g as immunostimulant for
   promoting wound healing.
PS Disclosure: fig 1; 13pp; German.
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CC Sequence encodes the human interleukin-1 alpha polypeptides of P90360.
CC CDS a encodes human IL-1 alpha, and CDS b encodes the above polypeptides.
CC See also P90108.
SQ Sequence 864 BP; 269 A; 196 C; 185 G; 214 T;

Query Match      100.0%; Score 9; DB 1; Length 864;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtca 9
   |||||
Db 350 TCTGAGTCA 342

RESULT 8
N90342
ID N90342 standard; DNA; 1569 BP.
AC N90342;
DE 1-NOV-1989 (first entry)
DE DNA of wild-type human adenovirus 3
KW Wild-type human adenovirus 3; DNA; E1A gene.
OS Adenovirus
FH Key Location/Qualifiers
FT misc_feature 745
   /*tag= a
FT enhancer 281..340
   /*tag= b
FT tata_signal 479..486
   /*tag= c
FT cds 575
   /*tag= d
FT misc_feature 1061..1255
   /*tag= e
FT misc_feature 1154..1255
   /*tag= f
FT misc_feature 1384..1389
   /*tag= g
FT terminator 1453
   /*tag= h
FT poly_a_signal 1494
   /*tag= i
FT misc_feature 1564
   /*tag= j
FT WO8906282-A.
PN 13-JUL-1989.
PD 03-JAN-1989; U00014.
PR 04-JAN-1988; US-140625.
PA (UYVA) Vanderbilt Univ.
PI Tibbets C, Larsen PL;
DR WPI: 89-220583/30.
DE Functional mutated E1A gene of human adenovirus
   - used to express E1A prods. that stimulate promoters
   controlling the E1A gene.
PS Disclosure: page 6-7; 24pp; English.
CC DNA of wild-type human adenovirus 3. The invention describes a mutant
   form with a modified autorepression functional domain (see N90343).
CC The features below are: a-BamHI; b-E1A promoter-proximal enhancer, the
   core of the enhancer starts at bp 304; e-12S mRNA splice junction; f-
   13S mRNA splice junction; g-HindIII; h-E1A gene translation stop; j-
   BglII. The deletion mutants can be formed by deletions at bp 956,
   974, 1000 and 1024, correspond to mutants dl13, dl7, dl1 and dl13 resp.
SQ Sequence 1569 BP; 397 A; 296 C; 430 G; 446 T;

Query Match      100.0%; Score 9; DB 1; Length 1569;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtca 9
   |||||
Db 317 TCTGAGTCA 325
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RESULT 9
ID N90343 standard; DNA; 1569 BP.
AC N90343;
DE 1-NOV-1989 (first entry)
KW Mutant human adenovirus Ad 3hr 15
KW modified autorepression; promoter; in-frame deletion; deletion.
OS Ad 3hr 15.
FH Key Location/Qualifiers
FT repeat 298..347
FT repeat /*tag= a
FT repeat 348..406
FT repeat /*tag= b
FT duplication 56..85
FT duplication /*tag= c
FT duplication 86-115
FT duplication /*tag= d
PN W08906282-A.
PD 13-JUL-1989.
PF 03-JAN-1989; U00014.
PR 04-JAN-1988; US-140625.
PA (UVVA) Vanderbilt Univ.
PI Tibbets C, Larsen PL;
DR WPI; 89-220583/30.
PT Functional mutated E1A gene of human adenovirus
PT - used to express E1A prods. that stimulate promoters
PT controlling the E1A gene.
PS Disclosure; page 10; 24pp; English.
CC DNA of mutant human Ad 3hr 15 has a modified autorepression functional
CC domain (see wild-type N90342) which can express E1A prods. that stimulate
CC without net repression of promoters controlling the mutated E1A gene.
CC The features below are: a and b-two tandem repeats of 60 bp - this
CC was the region shown to alter regulation of the E1A gene; c and d-
CC 30 bp duplications which are in the inverted terminal repeat. The
CC larger repeats are responsible for Ad 3h 15 altered regulation
CC (ATCC 53156).
SQ Sequence 1569 BP; 397 A; 296 C; 430 G; 446 T;

Query Match 100.0%; Score 9; DB 1; Length 1569;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtca 9
DB 317 TCTGAGTCA 325

RESULT 10
ID N92440 standard; DNA; 2120 BP.
AC N92440;
DE 30-APR-1990 (first entry)
DE DNA sequence encoding rat L-gulonolactone oxidase
KW Rat L-gulonolactone oxidase; rat liver.
OS Rat.
FH Key Location/Qualifiers
FT cds 24..1346
FT cds /*tag= a
PN J01091785-A.
PD 11-APR-1989.
PF 02-OCT-1987; JP-247896.
PR 02-OCT-1987; JP-247896.
PA (VITA-) Vitamin Kenkyusho K.
DR WPI; 89-148142/20.
DR P-FSD8; F91897.
PT Cloned DNA including rat L-gulonolactone oxidase
PT - used in recombinant vector for transforming host cells
PS Figure 2; 13pp; Japanese.
CC E. coli Y 1090 (r-) was transformed with cDNA expression library of
CC commercial lambda gtII phage prepd. from mRNA of rat liver. The clone
CC

CC containing L-gulonolactone oxidase was screened for and cultured. Its
CC DNA was digested with restriction enzyme and ligated into a vector which
CC was used to transform host cells which were then cultured to yield
CC L-gulonolactone oxidase, which was then separated and purified.
SQ Sequence 2120 BP; 481 A; 594 C; 546 G; 499 T;

Query Match 100.0%; Score 9; DB 1; Length 2120;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtca 9
DB 489 TCTGAGTCA 497

RESULT 11
ID N92768 standard; DNA; 9473 BP.
AC N92768;
DE 18-MAY-1990 (first entry)
DE HIV-2 variant HIV-D194 clone.
KW HIV-2; AIDS; HIV-D194; ss.
OS HIV-2.
PN EP-347365-A.
PD 20-DEC-1989.
PF 14-JUN-1988; 710057.
PR 14-JUN-1988; DE-820223.
PA (CHEM) Chemotherapeut Georg-Spe., (DIAG) Diagen.
PI Henco K, von Briesen H, Immelmann A, Kuhnelt H, Dietrich U, Rumsamen-,
PI Waigmann H, Adamski M;
DR WPI; 89-372573/51.
PT New HIV-2 virus variant isolates - used to obtain prods. for identifying
PT infections by HIV-2 or vaccines for protection against AIDS infections.
PS Disclosure; fig.4; 27pp; English.
CC The sequence characterises the clone HIV-D194, it starts with R/U5 region
CC of the ITR and ends with the U5 region. The DNA can be used to raise Abs
CC for serological detection, and polypeptides encoded by the sequence used
CC in vaccination.
SQ Sequence 9473 BP; 3215 A; 1953 C; 2374 G; 1923 T; 8 Others;

Query Match 100.0%; Score 9; DB 1; Length 9473;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtca 9
DB 7497 TCTGAGTCA 7489

RESULT 12
ID N90352 standard; DNA; 2100 BP.
AC N90352;
DE 12-DEC-1989 (first entry)
DE Sequence of plasmid pUC18GstPrt
KW pUC19GstPrt; HIV; gag gene; fusion protein; HIV protease.
OS Human immunodeficiency virus
FH Key Location/Qualifiers
FT cds 1..2097
FT cds /*tag= a
PN DE3800233-A.
PD 20-JUL-1989.
PF 07-JAN-1988; 00233.
PR 07-JAN-1988; DE-800233;
PA (WOLF) Hans Wolf.
PI Wolf H, Soutschek-Bauer E, Motz M;
DR WPI; 89-213869/30.
PT DNA coding for HIV protease and polypeptide precursor - useful for
PT screening for specific HIV protease inhibitors.
PS Disclosure; fig.5; page 25-28; 36pp; german.
CC The plasmid encodes a fusion protein comprising the amino acid sequences

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CC of N90350 and N90351 coupled to the protease. See P91051.
SQ Sequence 2100 BP; 756 A; 434 C; 495 G; 415 T;

Query Match 100.0%; Score 9; DB 1; Length 2100;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtca 9
|||||
Db 505 TCTGAGTCA 497

RESULT 13
N90353/c

ID N90353 standard; DNA; 1920 BP.

AC N90353;

DT 12-DEC-1989 (first entry)

DE Sequence of plasmid pUC18Gthprt

KW pUC18Gthprt; HIV; gag gene; fusion protein; HIV protease; ds.

OS Human immunodeficiency virus

FH Key Location/Qualifiers

FT cds 1..1920

FT /*tag= a

FT /label=gag precursor mol and protease

PN DE3800233-A.

PD 20-JUL-1989.

PF 07-JAN-1988; 000233.

PR 07-JAN-1988; DE-000233.

PA (WOLF) Hans Wolf.

PI Wolf H, Soutschek-Bauer E, Motz M;

DR WPI; 89-213869/30.

DR P-PSDB; P91051.

PT DNA coding for HIV protease and polypeptide precursor - useful for

PS screening for specific HIV protease inhibitors.

PS Disclosure; fig 5; page 25-28; 36pp; German.

CC Plasmid encodes a fusion protein comprising 435 amino acid residues of
the gag precursor mol. coupled to the protease. See also N90349, -50, -51
and -52.

CC and -52.

SQ Sequence 1920 BP; 706 A; 376 C; 456 G; 382 T;

Query Match

Best Local Similarity 100.0%; Score 9; DB 1; Length 1920;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtca 9

|||||
Db 505 TCTGAGTCA 497

RESULT 14
Q04043/c

ID Q04043 standard; cDNA; 4729 BP.

AC Q04043;

DT 07-SEP-1990 (first entry)

DE Recombinant DNA for alpha subunit of Mac-1 leukocyte adhesion receptor

KW Mac-1 alpha subunit; Mac-1 alpha/beta heterodimer; ssDNA

KW non-specific defence system; integrin gene superfamily.

OS synthetic.

FH Key Location/Qualifiers

FT poly_a_signal 4193..4198

FT /*tag= a

FT poly_a_signal 4684..4689

FT /*tag= b

FT cds 73..3532

FT /*tag= c

FT intron 3630..4070

FT /*tag= d

FT /label=boundaries of potential intron spliced out of

FT some of the cDNAs

PN EP-364690-A.

PD 25-APR-1990.

PF 17-AUG-1989; 115159.
PR 09-MAR-1989; US-321239.
PA (DANA-) Dana Farber Cancer.
PI Springer TA, Corbi A;
DR WPI; 90-125938/17.
DR P-PSDB; R04136.
PT New pure Mac-1 alpha sub-unit and corresp. DNA useful for treating
PT inflammation and viral infections ,and in diagnosis
PS Disclosure; p; English.
CC Mac-1 alpha subunit is involved in the response to inflammation, i.e.
CC recognition of and migration to sites of inflammation. They also attach
CC to cellular substrates as part of this function making them useful in
CC visualising endothelial tissue.
SQ Sequence 4729 BP; 1083 A; 1270 C; 1289 G; 1087 T;

Query Match 100.0%; Score 9; DB 1; Length 4729;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtca 9

|||||
Db 3897 TCTGAGTCA 3889

RESULT 15

Q05114/c

ID Q05114 standard; DNA; 402 BP.

AC Q05114;

DT 06-NOV-1990 (first entry)

DE HIV-1 protease gene from fragment of clone BH10.

KW HIV-1 protease; E.coli; galactokinase; HTLVIIIb; ds.

PN W09006369-A.

PD 14-JUN-1990.

PF 7-NOV-1989; 005009.

PR 9-DEC-1988; 282421.

PA (SMIT) Smithkline Beecham.

PI Debouck CM;

DR WPI; 90-209779/27.

DR P-PSDB; R05743.

PT Recombinant prodn. of mature protein prods. -

PT using host transformed with DNA encoding fusion protein with

PT protease cleavage site and DNA encoding protease.

PS Disclosure; English

CC Restriction enzyme, preferably retroviral, is cloned in a fusion

CC protein with the desired protein product, separated by a protease

CC cleavage site recognised by the encoded enzyme. The second portion

CC of the fusion protein may be an E.coli galactokinase gene segment.

SQ Sequence 402 BP; 144 A; 70 C; 89 G; 99 T;

Query Match

Best Local Similarity 100.0%; Score 9; DB 1; Length 402;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgagtca 9

|||||
Db 310 TCTGAGTCA 302

Search completed: June 24, 1999, 01:22:16

Job time: 2652 sec

